

SEQUENCE LISTING

<110> FRAZER, IAN HECTOR

<120> A METHOD FOR OPTIMISING GENE EXPRESSION USING SYNONYMOUS  
CODON OPTIMISATION

<130> 21415-0015US

<140> 10/534,130

<141> 2005-05-06

<150> PCT/AU03/01487

<151> 2003-11-10

<150> 60/425,163

<151> 2002-11-08

<160> 126

<170> PatentIn version 3.3

<210> 1

<211> 714

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
humanized GFP sequence

<220>

<221> CDS

<222> (1)..(711)

<400> 1

agc aag ggc gag gaa ctg ttc act ggc gtg gtc cca att ctc gtg gaa	48
Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val Glu	
1 5 10 15	
ctg gat ggc gat gtg aat ggg cac aaa ttt tct gtc agc gga gag ggt	96
Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu Gly	
20 25 30	
gaa ggt gat gcc aca tac gga aag ctc acc ctg aaa ttc atc tgc acc	144
Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys Thr	
35 40 45	
act gga aag ctc cct gtg cca tgg cca aca ctg gtc act acc ttc tct	192
Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Phe Ser	
50 55 60	
tat ggc gtg cag tgc ttt tcc aga tac cca gac cat atg aag cag cat	240
Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro Asp His Met Lys Gln His	
65 70 75 80	

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gac ttt ttc aag agc gcc atg ccc gag ggc tat gtg cag gag aga acc      288
Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg Thr
      85                      90                      95

atc ttt ttc aaa gat gac ggg aac tac aag acc cgc gct gaa gtc aag      336
Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys
      100                      105                      110

ttc gaa ggt gac acc ctg gtg aat aga atc gag ctg aag ggc att gac      384
Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp
      115                      120                      125

ttt aag gag gat gga aac att ctc ggc cac aag ctg gaa tac aac tat      432
Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr
      130                      135                      140

aac tcc cac aat gtg tac atc atg gcc gac aag caa aag aat ggc atc      480
Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly Ile
      145                      150                      155                      160

aag gtc aac ttc aag atc aga cac aac att gag gat gga tcc gtg cag      528
Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser Val Gln
      165                      170                      175

ctg gcc gac cat tat caa cag aac act cca atc ggc gac ggc cct gtg      576
Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val
      180                      185                      190

ctc ctc cca gac aac cat tac ctg tcc acc cag tct gcc ctg tct aaa      624
Leu Leu Pro Asp Asn His Tyr Leu Ser Thr Gln Ser Ala Leu Ser Lys
      195                      200                      205

gat ccc aac gaa aag aga gac cac atg gtc ctg ctg gag ttt gtg acc      672
Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu Glu Phe Val Thr
      210                      215                      220

gct gct ggg atc aca cat ggc atg gac gag ctg tac aag tga      714
Ala Ala Gly Ile Thr His Gly Met Asp Glu Leu Tyr Lys
      225                      230                      235

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<213> Artificial Sequence

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<223> Description of Artificial Sequence: Synthetic  
humanized GFP sequence

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Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val Glu
1                      5                      10                      15

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Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu Gly
      20                      25                      30

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Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys Thr  
 35 40 45

Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Phe Ser  
 50 55 60

Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro Asp His Met Lys Gln His  
 65 70 75 80

Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg Thr  
 85 90 95

Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys  
 100 105 110

Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp  
 115 120 125

Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr  
 130 135 140

Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly Ile  
 145 150 155 160

Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser Val Gln  
 165 170 175

Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val  
 180 185 190

Leu Leu Pro Asp Asn His Tyr Leu Ser Thr Gln Ser Ala Leu Ser Lys  
 195 200 205

Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu Glu Phe Val Thr  
 210 215 220

Ala Ala Gly Ile Thr His Gly Met Asp Glu Leu Tyr Lys  
 225 230 235

<210> 3

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<212> DNA

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<220>  
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 leader sequence

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<400> 3  
 gca gca gca gca gca gca  
 Ala Ala Ala Ala Ala Ala  
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 Ala Ala Ala Ala Ala Ala  
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 Ala Ala Ala Ala Ala Ala  
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Ala Ala Ala Ala Ala Ala  
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<400> 9  
gcc gcc gcc gcc gcc gcc  
Ala Ala Ala Ala Ala Ala  
1 5

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<400> 10  
 Ala Ala Ala Ala Ala Ala  
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 aga aga aga aga aga aga  
 Arg Arg Arg Arg Arg Arg  
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 Arg Arg Arg Arg Arg Arg  
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 Arg Arg Arg Arg Arg Arg  
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 Arg Arg Arg Arg Arg Arg  
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<400> 16  
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 Arg Arg Arg Arg Arg Arg  
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<400> 19  
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 Arg Arg Arg Arg Arg Arg  
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<400> 20  
 Arg Arg Arg Arg Arg Arg  
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 Arg Arg Arg Arg Arg Arg  
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<400> 22  
 Arg Arg Arg Arg Arg Arg  
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<400> 23  
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 Asn Asn Asn Asn Asn Asn  
 1 5

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<400> 24  
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<400> 25  
 aat aat aat aat aat aat  
 Asn Asn Asn Asn Asn Asn  
 1 5

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<400> 26  
 Asn Asn Asn Asn Asn Asn  
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 leader sequence

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<400> 27  
 gat gat gat gat gat gat  
 Asp Asp Asp Asp Asp Asp  
 1 5

18

<210> 28  
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 leader sequence

<400> 28  
 Asp Asp Asp Asp Asp Asp  
 1 5

<210> 29  
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 gac gac gac gac gac gac  
 Asp Asp Asp Asp Asp Asp  
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18

<210> 30  
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<400> 30  
 Asp Asp Asp Asp Asp Asp  
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<210> 31  
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 leader sequence

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 tgc tgc tgc tgc tgc tgc  
 Cys Cys Cys Cys Cys Cys  
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 leader sequence

<400> 32  
 Cys Cys Cys Cys Cys Cys  
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<210> 33  
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 leader sequence

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<400> 33  
 tgt tgt tgt tgt tgt tgt  
 Cys Cys Cys Cys Cys Cys  
 1 5

18

<210> 34  
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 Cys Cys Cys Cys Cys Cys  
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 Gln Gln Gln Gln Gln Gln  
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 Gln Gln Gln Gln Gln Gln  
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 Gln Gln Gln Gln Gln Gln  
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<210> 38  
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 leader sequence

<400> 38  
 Gln Gln Gln Gln Gln Gln  
 1 5

<210> 39  
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 leader sequence

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<400> 39  
 gaa gaa gaa gaa gaa gaa  
 Glu Glu Glu Glu Glu Glu  
 1 5

18

<210> 40  
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 leader sequence

<400> 40  
 Glu Glu Glu Glu Glu Glu  
 1 5

<210> 41  
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 leader sequence

<220>  
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<400> 41  
 gag gag gag gag gag gag  
 Glu Glu Glu Glu Glu Glu  
 1 5

18

<210> 42  
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<220>  
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 leader sequence

<400> 42  
 Glu Glu Glu Glu Glu Glu  
 1 5

<210> 43  
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<220>  
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 leader sequence

<220>  
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<400> 43  
 gga gga gga gga gga gga  
 Gly Gly Gly Gly Gly Gly  
 1 5

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<210> 44  
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<400> 44  
 Gly Gly Gly Gly Gly Gly  
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 leader sequence

<220>  
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 Gly Gly Gly Gly Gly Gly  
 1 5

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<210> 46  
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 leader sequence

<400> 46  
 Gly Gly Gly Gly Gly Gly  
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<210> 47  
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<400> 47  
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 Gly Gly Gly Gly Gly Gly  
 1 5

18

<210> 48  
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 leader sequence

<400> 48  
 Gly Gly Gly Gly Gly Gly  
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<400> 49  
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 Gly Gly Gly Gly Gly Gly  
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<210> 50  
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<400> 50  
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<210> 51  
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 leader sequence

<220>  
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<400> 51  
 cac cac cac cac cac cac  
 His His His His His His  
 1 5

18

<210> 52  
 <211> 6  
 <212> PRT  
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 leader sequence

<400> 52  
 His His His His His His  
 1 5

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 leader sequence

<220>  
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<400> 53  
 cat cat cat cat cat cat  
 His His His His His His  
 1 5

18

<210> 54  
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 leader sequence

<400> 54  
 His His His His His His  
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<210> 55  
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<400> 55  
 atc atc atc atc atc atc  
 Ile Ile Ile Ile Ile Ile  
 1 5

18

<210> 56  
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<220>  
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 leader sequence

<400> 56  
 Ile Ile Ile Ile Ile Ile  
 1 5

<210> 57  
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<220>  
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 leader sequence

<220>  
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<400> 57  
 att att att att att att  
 Ile Ile Ile Ile Ile Ile  
 1 5

18

<210> 58  
 <211> 6  
 <212> PRT  
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<220>  
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 leader sequence

<400> 58  
 Ile Ile Ile Ile Ile Ile  
 1 5

<210> 59  
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<220>  
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 leader sequence

<220>  
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<400> 59  
 ata ata ata ata ata ata  
 Ile Ile Ile Ile Ile Ile  
 1 5

18

<210> 60  
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<400> 60  
 Ile Ile Ile Ile Ile Ile  
 1 5

<210> 61  
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<220>  
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 leader sequence

<220>  
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<400> 61  
 ctc ctc ctc ctc ctc ctc  
 Leu Leu Leu Leu Leu Leu  
 1 5

18

<210> 62  
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<220>  
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 leader sequence

<400> 62  
 Leu Leu Leu Leu Leu Leu  
 1 5

<210> 63  
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<220>  
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 leader sequence

<220>  
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 <222> (1)..(18)

<400> 63  
 ttg ttg ttg ttg ttg ttg  
 Leu Leu Leu Leu Leu Leu  
 1 5

18

<210> 64  
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 <212> PRT  
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<220>  
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 leader sequence

<400> 64  
 Leu Leu Leu Leu Leu Leu  
 1 5

<210> 65  
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 leader sequence

<220>  
 <221> CDS  
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<400> 65  
 cta cta cta cta cta cta  
 Leu Leu Leu Leu Leu Leu  
 1 5

18

<210> 66  
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<220>  
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 leader sequence

<400> 66  
 Leu Leu Leu Leu Leu Leu  
 1 5

<210> 67  
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<220>  
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 leader sequence

<220>  
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<400> 67  
 ctg ctg ctg ctg ctg ctg  
 Leu Leu Leu Leu Leu Leu  
 1 5

18

<210> 68  
 <211> 6  
 <212> PRT  
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<220>  
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 leader sequence

<400> 68  
 Leu Leu Leu Leu Leu Leu  
 1 5

<210> 69  
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<220>  
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 leader sequence

<220>  
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 <222> (1)..(18)

<400> 69  
 tta tta tta tta tta tta  
 Leu Leu Leu Leu Leu Leu  
 1 5

18

<210> 70  
 <211> 6  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic  
 leader sequence

<400> 70  
 Leu Leu Leu Leu Leu Leu  
 1 5

<210> 71  
 <211> 18  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic  
 leader sequence

<220>  
 <221> CDS  
 <222> (1)..(18)

<400> 71  
 ctt ctt ctt ctt ctt ctt  
 Leu Leu Leu Leu Leu Leu  
 1 5

18

<210> 72  
 <211> 6  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic  
 leader sequence

<400> 72  
 Leu Leu Leu Leu Leu Leu  
 1 5

<210> 73  
 <211> 18  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic  
 leader sequence

<220>  
 <221> CDS  
 <222> (1)..(18)

<400> 73  
 aag aag aag aag aag aag  
 Lys Lys Lys Lys Lys Lys  
 1 5

18

<210> 74  
 <211> 6  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic  
 leader sequence

<400> 74  
 Lys Lys Lys Lys Lys Lys  
 1 5

<210> 75  
 <211> 18  
 <212> DNA  
 <213> Artificial Sequence



<220>  
 <223> Description of Artificial Sequence: Synthetic  
 leader sequence

<220>  
 <221> CDS  
 <222> (1)..(18)

<400> 75  
 aaa aaa aaa aaa aaa aaa  
 Lys Lys Lys Lys Lys Lys  
 1 5

18

<210> 76  
 <211> 6  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic  
 leader sequence

<400> 76  
 Lys Lys Lys Lys Lys Lys  
 1 5

<210> 77  
 <211> 18  
 <212> DNA  
 <213> Artificial sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic  
 leader sequence

<220>  
 <221> CDS  
 <222> (1)..(18)

<400> 77  
 ttt ttt ttt ttt ttt ttt  
 Phe Phe Phe Phe Phe Phe  
 1 5

18

<210> 78  
 <211> 6  
 <212> PRT  
 <213> Artificial sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic  
 leader sequence

<400> 78  
 Phe Phe Phe Phe Phe Phe  
 1 5

<210> 79  
 <211> 18  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic  
 leader sequence

<220>  
 <221> CDS  
 <222> (1)..(18)

<400> 79  
 ttc ttc ttc ttc ttc ttc  
 Phe Phe Phe Phe Phe Phe  
 1 5

18

<210> 80  
 <211> 6  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic  
 leader sequence

<400> 80  
 Phe Phe Phe Phe Phe Phe  
 1 5

<210> 81  
 <211> 18  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic  
 leader sequence

<220>  
 <221> CDS  
 <222> (1)..(18)

<400> 81  
 ccc ccc ccc ccc ccc ccc  
 Pro Pro Pro Pro Pro Pro  
 1 5

18

<210> 82  
 <211> 6  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic  
 leader sequence

<400> 82  
 Pro Pro Pro Pro Pro Pro  
 1 5

<210> 83  
 <211> 18  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic  
 leader sequence

<220>  
 <221> CDS  
 <222> (1)..(18)

<400> 83  
 cct cct cct cct cct cct  
 Pro Pro Pro Pro Pro Pro  
 1 5

18

<210> 84  
 <211> 6  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic  
 leader sequence

<400> 84  
 Pro Pro Pro Pro Pro Pro  
 1 5

<210> 85  
 <211> 18  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic  
 leader sequence

<220>  
 <221> CDS  
 <222> (1)..(18)

<400> 85  
 ccg ccg ccg ccg ccg ccg  
 Pro Pro Pro Pro Pro Pro  
 1 5

18

<210> 86  
 <211> 6  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic  
 leader sequence

<400> 86  
 Pro Pro Pro Pro Pro Pro  
 1 5

<210> 87  
 <211> 18  
 <212> DNA  
 <213> Artificial sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic  
 leader sequence

<220>  
 <221> CDS  
 <222> (1)..(18)

<400> 87  
 cca cca cca cca cca cca  
 Pro Pro Pro Pro Pro Pro  
 1 5

18

<210> 88  
 <211> 6  
 <212> PRT  
 <213> Artificial sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic  
 leader sequence

<400> 88  
 Pro Pro Pro Pro Pro Pro  
 1 5

<210> 89  
 <211> 18  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic  
 leader sequence

<220>  
 <221> CDS  
 <222> (1)..(18)

<400> 89  
 agc agc agc agc agc agc  
 Ser Ser Ser Ser Ser Ser  
 1 5

18

<210> 90  
 <211> 6  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic  
 leader sequence

<400> 90  
 Ser Ser Ser Ser Ser Ser  
 1 5

<210> 91  
 <211> 18  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic  
 leader sequence

<220>  
 <221> CDS  
 <222> (1)..(18)

<400> 91  
 tct tct tct tct tct tct  
 Ser Ser Ser Ser Ser Ser  
 1 5

18

<210> 92  
 <211> 6  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic  
 leader sequence

<400> 92  
 Ser Ser Ser Ser Ser Ser  
 1 5

<210> 93  
 <211> 18  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic  
 leader sequence

<220>  
 <221> CDS  
 <222> (1)..(18)

<400> 93  
 agt agt agt agt agt agt  
 Ser Ser Ser Ser Ser Ser  
 1 5

18

<210> 94  
 <211> 6  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic  
 leader sequence

<400> 94  
 Ser Ser Ser Ser Ser Ser  
 1 5

<210> 95  
 <211> 18  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic  
 leader sequence

<220>  
 <221> CDS  
 <222> (1)..(18)

<400> 95  
 tcg tcg tcg tcg tcg tcg  
 Ser Ser Ser Ser Ser Ser  
 1 5

18

<210> 96  
 <211> 6  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic  
 leader sequence

<400> 96  
 Ser Ser Ser Ser Ser Ser  
 1 5

<210> 97  
 <211> 18  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic  
 leader sequence

<220>  
 <221> CDS  
 <222> (1)..(18)

<400> 97  
 tca tca tca tca tca tca  
 Ser Ser Ser Ser Ser Ser  
 1 5

18

<210> 98  
 <211> 6  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic  
 leader sequence

<400> 98  
 Ser Ser Ser Ser Ser Ser  
 1 5

<210> 99  
 <211> 18  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic  
 leader sequence

<220>  
 <221> CDS  
 <222> (1)..(18)

<400> 99  
 tcc tcc tcc tcc tcc tcc  
 Ser Ser Ser Ser Ser Ser  
 1 5

18

<210> 100  
 <211> 6  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic  
 leader sequence

<400> 100  
 Ser Ser Ser Ser Ser Ser  
 1 5

<210> 101  
 <211> 18  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic  
 leader sequence

<220>  
 <221> CDS  
 <222> (1)..(18)

<400> 101  
 aca aca aca aca aca aca  
 Thr Thr Thr Thr Thr Thr  
 1 5

18

<210> 102  
 <211> 6  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic  
 leader sequence



<400> 102  
 Thr Thr Thr Thr Thr Thr  
 1 5

<210> 103  
 <211> 18  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic  
 leader sequence

<220>  
 <221> CDS  
 <222> (1)..(18)

<400> 103  
 acg acg acg acg acg acg  
 Thr Thr Thr Thr Thr Thr  
 1 5

18

<210> 104  
 <211> 6  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic  
 leader sequence

<400> 104  
 Thr Thr Thr Thr Thr Thr  
 1 5

<210> 105  
 <211> 18  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic  
 leader sequence

<220>  
 <221> CDS  
 <222> (1)..(18)

<400> 105  
 act act act act act act  
 Thr Thr Thr Thr Thr Thr  
 1 5

18

<210> 106  
 <211> 6  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic  
 leader sequence

<400> 106  
 Thr Thr Thr Thr Thr Thr  
 1 5

<210> 107  
 <211> 18  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic  
 leader sequence

<220>  
 <221> CDS  
 <222> (1)..(18)

<400> 107  
 acc acc acc acc acc acc  
 Thr Thr Thr Thr Thr Thr  
 1 5

18

<210> 108  
 <211> 6  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic  
 leader sequence

<400> 108  
 Thr Thr Thr Thr Thr Thr  
 1 5

<210> 109  
 <211> 18  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic  
 leader sequence

<220>  
 <221> CDS  
 <222> (1)..(18)

<400> 109  
 tac tac tac tac tac tac  
 Tyr Tyr Tyr Tyr Tyr Tyr  
 1 5

18

<210> 110  
 <211> 6  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic  
 leader sequence

<400> 110  
 Tyr Tyr Tyr Tyr Tyr Tyr  
 1 5

<210> 111  
 <211> 18  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic  
 leader sequence

<220>  
 <221> CDS  
 <222> (1)..(18)

<400> 111  
 tat tat tat tat tat tat  
 Tyr Tyr Tyr Tyr Tyr Tyr  
 1 5

18

<210> 112  
 <211> 6  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic  
 leader sequence

<400> 112  
 Tyr Tyr Tyr Tyr Tyr Tyr  
 1 5

<210> 113  
 <211> 18  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic  
 leader sequence

<220>  
 <221> CDS  
 <222> (1)..(18)

<400> 113  
 gtg gtg gtg gtg gtg gtg  
 Val Val Val Val Val Val  
 1 5

18

<210> 114  
 <211> 6  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic  
 leader sequence

<400> 114  
 Val Val Val Val Val Val  
 1 5

<210> 115  
 <211> 18  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic  
 leader sequence

<220>  
 <221> CDS  
 <222> (1)..(18)

<400> 115  
 gtt gtt gtt gtt gtt gtt  
 Val Val Val Val Val Val  
 1 5

18

<210> 116  
 <211> 6  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic  
 leader sequence

<400> 116  
 Val Val Val Val Val Val  
 1 5

<210> 117  
 <211> 18  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic  
 leader sequence

<220>  
 <221> CDS  
 <222> (1)..(18)

<400> 117  
 gtc gtc gtc gtc gtc gtc  
 Val Val Val Val Val Val  
 1 5

18

<210> 118  
 <211> 6  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic  
 leader sequence

<400> 118  
 Val Val Val Val Val Val  
 1 5

<210> 119  
 <211> 18  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic  
 leader sequence

<220>  
 <221> CDS  
 <222> (1)..(18)

&lt;400&gt; 119

gta gta gta gta gta gta  
 Val Val Val Val Val Val  
 1 5

18

&lt;210&gt; 120

&lt;211&gt; 6

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

<223> Description of Artificial Sequence: Synthetic  
 leader sequence

&lt;400&gt; 120

Val Val Val Val Val Val  
 1 5

&lt;210&gt; 121

&lt;211&gt; 2583

&lt;212&gt; DNA

&lt;213&gt; Mus sp.

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (1)..(2166)

&lt;400&gt; 121

gaa ctt cgg gac gag caa act ccg ggc cac agg aag aac cca tcg aac 48  
 Glu Leu Arg Asp Glu Gln Thr Pro Gly His Arg Lys Asn Pro Ser Asn  
 1 5 10 15

caa agc agc tta gaa tct gac tcc aat tac ccc tcc att tcc act tcc 96  
 Gln Ser Ser Leu Glu Ser Asp Ser Asn Tyr Pro Ser Ile Ser Thr Ser  
 20 25 30

gaa atc gga gac act gag gat gcc ctt cag cag gtg gag gag att ggc 144  
 Glu Ile Gly Asp Thr Glu Asp Ala Leu Gln Gln Val Glu Glu Ile Gly  
 35 40 45

ata gag aag gca gcc atg gac atg acc gtc ttc ctg aag ctg cag aag 192  
 Ile Glu Lys Ala Ala Met Asp Met Thr Val Phe Leu Lys Leu Gln Lys  
 50 55 60

aga gtg cgc gaa ctt gag cag gag agg aag aag ctg cag gcg cag cta 240  
 Arg Val Arg Glu Leu Glu Gln Glu Arg Lys Lys Leu Gln Ala Gln Leu  
 65 70 75 80

gaa aag gga cag cag gac agc aag aaa ggg cag gta gaa caa cag aac 288  
 Glu Lys Gly Gln Gln Asp Ser Lys Lys Gly Gln Val Glu Gln Gln Asn  
 85 90 95

aat ggc tta gat gtg gac cag gac gca gat ata gcc tac aat agt ctg 336  
 Asn Gly Leu Asp Val Asp Gln Asp Ala Asp Ile Ala Tyr Asn Ser Leu  
 100 105 110

aag aga cag gag ctt gag tca gag aac aag aag ctg aag aat gac ctg Lys Arg Gln Glu Leu Glu Ser Glu Asn Lys Lys Leu Lys Asn Asp Leu 115 120 125	384
aat gag ctg agg aac ggt gtc gct gac caa gcc atg cag gat aac tcc Asn Glu Leu Arg Asn Gly Val Ala Asp Gln Ala Met Gln Asp Asn Ser 130 135 140	432
acc cac agc tcc cca gac agc tac agc ctc cta ctg aac cag ctc aag Thr His Ser Ser Pro Asp Ser Tyr Ser Leu Leu Leu Asn Gln Leu Lys 145 150 155 160	480
ctg gcc aat gag gag ctc gag gtc cgc aaa gag gag gcg ctg atc ctc Leu Ala Asn Glu Glu Leu Glu Val Arg Lys Glu Glu Ala Leu Ile Leu 165 170 175	528
agg acc cag atc atg aat gcc gac cag cgc cgc ctg tct ggc aag aac Arg Thr Gln Ile Met Asn Ala Asp Gln Arg Arg Leu Ser Gly Lys Asn 180 185 190	576
atg gag ccg aac atc aat gcc aga aca agt tgg ccc aac agt gag aag Met Glu Pro Asn Ile Asn Ala Arg Thr Ser Trp Pro Asn Ser Glu Lys 195 200 205	624
cac gtg gac cag gaa gac gcc att gag gcc tat cac ggg gtc tgc cag His Val Asp Gln Glu Asp Ala Ile Glu Ala Tyr His Gly Val Cys Gln 210 215 220	672
aca aac agg ttg ctg gag gcc cag ctg cag gcc cag agc ctg gag cat Thr Asn Arg Leu Leu Glu Ala Gln Leu Gln Ala Gln Ser Leu Glu His 225 230 235 240	720
gag gag gag gtg gaa cat ctc aag gcc cag gtg gaa gcc ctg aaa gag Glu Glu Glu Val Glu His Leu Lys Ala Gln Val Glu Ala Leu Lys Glu 245 250 255	768
gag atg gac aaa cag cag cag acc ttc tgc cag acc ctg ctg ctc tcc Glu Met Asp Lys Gln Gln Gln Thr Phe Cys Gln Thr Leu Leu Leu Ser 260 265 270	816
cca gag gcc cag gta gaa ttt ggt gtc cag cag gag ata tcc cgg ctg Pro Glu Ala Gln Val Glu Phe Gly Val Gln Gln Glu Ile Ser Arg Leu 275 280 285	864
acc aat gag aac ctg gat ttt aag gaa ttg gtg gaa aag ctg gag aag Thr Asn Glu Asn Leu Asp Phe Lys Glu Leu Val Glu Lys Leu Glu Lys 290 295 300	912
aat gag agg aag ctg aag aag cag ctg aag att tac atg aag aag gtc Asn Glu Arg Lys Leu Lys Lys Gln Leu Lys Ile Tyr Met Lys Lys Val 305 310 315 320	960
cag gac tta gaa gct gcc cag gcg ttg gca cag agt gac agg agg cac Gln Asp Leu Glu Ala Ala Gln Ala Leu Ala Gln Ser Asp Arg Arg His 325 330 335	1008

cat gaa ctc aca aga cag gtc aca gtc caa cga aaa gag aag gac ttc His Gln Leu Thr Arg Gln Val Thr Val Gln Arg Lys Glu Lys Asp Phe 340 345 350	1056
caa ggc atg ctg gag tac cac aaa gag gtc gaa gcc ctc ctc atc cgg Gln Gly Met Leu Glu Tyr His Lys Glu Val Glu Ala Leu Leu Ile Arg 355 360 365	1104
aac ctg gtg aca gac ctg aag cct cag atg ctg ctg ggc acc gtg ccc Asn Leu Val Thr Asp Leu Lys Pro Gln Met Leu Leu Gly Thr Val Pro 370 375 380	1152
tgt ctg cct gca tac ata ctc tat atg tgc atc agg cac gcg gat tac Cys Leu Pro Ala Tyr Ile Leu Tyr Met Cys Ile Arg His Ala Asp Tyr 385 390 395 400	1200
acc aac gat gac ctc aag gtg cac tcg ttg ctg agc tcc acc atc aac Thr Asn Asp Asp Leu Lys Val His Ser Leu Leu Ser Ser Thr Ile Asn 405 410 415	1248
ggc att aag aaa gtc ctc aag aag cac aat gac gac ttt gag atg acg Gly Ile Lys Lys Val Leu Lys Lys His Asn Asp Asp Phe Glu Met Thr 420 425 430	1296
tca ttc tgg tta tcc aac acc tgc cgc ttc ctt cac tgt ctg aag caa Ser Phe Trp Leu Ser Asn Thr Cys Arg Phe Leu His Cys Leu Lys Gln 435 440 445	1344
tac agt ggt gat gag ggt ttc atg aca cag aac atc gcg aag cag aat Tyr Ser Gly Asp Glu Gly Phe Met Thr Gln Asn Ile Ala Lys Gln Asn 450 455 460	1392
gag cac tgt ctc aag aac ttt gac ctc act gaa tac cgc cag gta cta Glu His Cys Leu Lys Asn Phe Asp Leu Thr Glu Tyr Arg Gln Val Leu 465 470 475 480	1440
agc gac ctt tcc att cag atc tat cag cag ctc att aaa atg ccc gag Ser Asp Leu Ser Ile Gln Ile Tyr Gln Gln Leu Ile Lys Met Pro Glu 485 490 495	1488
ggc ttg cta cag cct atg ata gtt tct gcc atg ttg gaa aat gag agt Gly Leu Leu Gln Pro Met Ile Val Ser Ala Met Leu Glu Asn Glu Ser 500 505 510	1536
atc cag ggg ctg tct ggt gtg aga cca act ggt tac cgg aag cgc tcc Ile Gln Gly Leu Ser Gly Val Arg Pro Thr Gly Tyr Arg Lys Arg Ser 515 520 525	1584
tcc agc atg gtg gat gga gag aat tct ttc cat aca gtc ctg tgt gac Ser Ser Met Val Asp Gly Glu Asn Ser Phe His Thr Val Leu Cys Asp 530 535 540	1632
cag ggc ctg gac ccc gag att atc ctg cag gtg ttc aaa cag ctc ttc Gln Gly Leu Asp Pro Glu Ile Ile Leu Gln Val Phe Lys Gln Leu Phe 545 550 555 560	1680



tac atg atc aat gct gtg act ctt aac aac cta ctc ctg cgg aaa gac	1728
Tyr Met Ile Asn Ala Val Thr Leu Asn Asn Leu Leu Leu Arg Lys Asp	
565 570 575	
gcc tgc tcc tgg agc aca ggc atg caa ctc agg tac aac ata agt caa	1776
Ala Cys Ser Trp Ser Thr Gly Met Gln Leu Arg Tyr Asn Ile Ser Gln	
580 585 590	
ctg gaa gag tgg ctt cgg ggc aaa aac ctt cac cag agt gga gca gtt	1824
Leu Glu Glu Trp Leu Arg Gly Lys Asn Leu His Gln Ser Gly Ala Val	
595 600 605	
cag acc atg gag ccc ctg atc cag gca gcc cag ctc ctc cag ctg aag	1872
Gln Thr Met Glu Pro Leu Ile Gln Ala Ala Gln Leu Leu Gln Leu Lys	
610 615 620	
aag aaa acc cac gag gat gct gag gcc atc tgc tct ctg tgc acc tcc	1920
Lys Lys Thr His Glu Asp Ala Glu Ala Ile Cys Ser Leu Cys Thr Ser	
625 630 635 640	
ctc agc acc cag cag att gtc aaa att tta aac ctc tac act ccc ttg	1968
Leu Ser Thr Gln Gln Ile Val Lys Ile Leu Asn Leu Tyr Thr Pro Leu	
645 650 655	
aat gaa ttt gag gaa cgg gtc aca gtg tcc ttc atc aga aca atc cag	2016
Asn Glu Phe Glu Glu Arg Val Thr Val Ser Phe Ile Arg Thr Ile Gln	
660 665 670	
gct cag cta caa gag agg aat gac cct cag cag ctc ctg ctg gac tcc	2064
Ala Gln Leu Gln Glu Arg Asn Asp Pro Gln Gln Leu Leu Leu Asp Ser	
675 680 685	
aag cac gtg ttc cca gtt ctg ttt cca tat aac cca tct gct ctg acc	2112
Lys His Val Phe Pro Val Leu Phe Pro Tyr Asn Pro Ser Ala Leu Thr	
690 695 700	
atg gac tcg atc cac atc ccg gcc tgt ctc aac ctg gag ttt ctc aat	2160
Met Asp Ser Ile His Ile Pro Ala Cys Leu Asn Leu Glu Phe Leu Asn	
705 710 715 720	
gaa gtc tgaggatgcg tgtttccgag gcgagcgaga aggaagcatg tgctgtcagc	2216
Glu Val	
cgagagaatg ctaggtgtgt taaatattcc agcgtagatc aaaccatggt agagactggc	2276
gggacgacag aactaaacag cgggggtgcac agttgtcgcc aatgctgctc agaaaacacc	2336
cggaagtgga tttgttaaag ctgtgctttc aggttaaacc aagacacgtc agaacgaaca	2396
gccactctgc agctccagtc gccatataaa aatgccagtt ctacagagtg gaagtgccta	2456
gctttgatct ttgtatatat cttgagaatg ttcaaactga gataatatta aaaacacatg	2516
acgtaaattg cctttgtggg tctttcaaga aatgatggga ctaataacca taagattgac	2576
aggaatt	2583

&lt;210&gt; 122

&lt;211&gt; 722

&lt;212&gt; PRT

&lt;213&gt; Mus sp.

&lt;400&gt; 122

Glu Leu Arg Asp Glu Gln Thr Pro Gly His Arg Lys Asn Pro Ser Asn  
 1 5 10 15

Gln Ser Ser Leu Glu Ser Asp Ser Asn Tyr Pro Ser Ile Ser Thr Ser  
 20 25 30

Glu Ile Gly Asp Thr Glu Asp Ala Leu Gln Gln Val Glu Glu Ile Gly  
 35 40 45

Ile Glu Lys Ala Ala Met Asp Met Thr Val Phe Leu Lys Leu Gln Lys  
 50 55 60

Arg Val Arg Glu Leu Glu Gln Glu Arg Lys Lys Leu Gln Ala Gln Leu  
 65 70 75 80

Glu Lys Gly Gln Gln Asp Ser Lys Lys Gly Gln Val Glu Gln Gln Asn  
 85 90 95

Asn Gly Leu Asp Val Asp Gln Asp Ala Asp Ile Ala Tyr Asn Ser Leu  
 100 105 110

Lys Arg Gln Glu Leu Glu Ser Glu Asn Lys Lys Leu Lys Asn Asp Leu  
 115 120 125

Asn Glu Leu Arg Asn Gly Val Ala Asp Gln Ala Met Gln Asp Asn Ser  
 130 135 140

Thr His Ser Ser Pro Asp Ser Tyr Ser Leu Leu Leu Asn Gln Leu Lys  
 145 150 155 160

Leu Ala Asn Glu Glu Leu Glu Val Arg Lys Glu Glu Ala Leu Ile Leu  
 165 170 175

Arg Thr Gln Ile Met Asn Ala Asp Gln Arg Arg Leu Ser Gly Lys Asn  
 180 185 190

Met Glu Pro Asn Ile Asn Ala Arg Thr Ser Trp Pro Asn Ser Glu Lys  
 195 200 205

His Val Asp Gln Glu Asp Ala Ile Glu Ala Tyr His Gly Val Cys Gln  
 210 215 220

Thr Asn Arg Leu Leu Glu Ala Gln Leu Gln Ala Gln Ser Leu Glu His  
 225 230 235 240

Glu Glu Glu Val Glu His Leu Lys Ala Gln Val Glu Ala Leu Lys Glu  
 245 250 255

Glu Met Asp Lys Gln Gln Gln Thr Phe Cys Gln Thr Leu Leu Leu Ser  
 260 265 270

Pro Glu Ala Gln Val Glu Phe Gly Val Gln Gln Glu Ile Ser Arg Leu  
 275 280 285

Thr Asn Glu Asn Leu Asp Phe Lys Glu Leu Val Glu Lys Leu Glu Lys  
 290 295 300

Asn Glu Arg Lys Leu Lys Lys Gln Leu Lys Ile Tyr Met Lys Lys Val  
 305 310 315 320

Gln Asp Leu Glu Ala Ala Gln Ala Leu Ala Gln Ser Asp Arg Arg His  
 325 330 335

His Glu Leu Thr Arg Gln Val Thr Val Gln Arg Lys Glu Lys Asp Phe  
 340 345 350

Gln Gly Met Leu Glu Tyr His Lys Glu Val Glu Ala Leu Leu Ile Arg  
 355 360 365

Asn Leu Val Thr Asp Leu Lys Pro Gln Met Leu Leu Gly Thr Val Pro  
 370 375 380

Cys Leu Pro Ala Tyr Ile Leu Tyr Met Cys Ile Arg His Ala Asp Tyr  
 385 390 395 400

Thr Asn Asp Asp Leu Lys Val His Ser Leu Leu Ser Ser Thr Ile Asn  
 405 410 415

Gly Ile Lys Lys Val Leu Lys Lys His Asn Asp Asp Phe Glu Met Thr  
 420 425 430

Ser Phe Trp Leu Ser Asn Thr Cys Arg Phe Leu His Cys Leu Lys Gln  
 435 440 445

Tyr Ser Gly Asp Glu Gly Phe Met Thr Gln Asn Ile Ala Lys Gln Asn  
 450 455 460

Glu His Cys Leu Lys Asn Phe Asp Leu Thr Glu Tyr Arg Gln Val Leu  
 465 470 475 480

Ser Asp Leu Ser Ile Gln Ile Tyr Gln Gln Leu Ile Lys Met Pro Glu  
 485 490 495

Gly Leu Leu Gln Pro Met Ile Val Ser Ala Met Leu Glu Asn Glu Ser  
 500 505 510

Ile Gln Gly Leu Ser Gly Val Arg Pro Thr Gly Tyr Arg Lys Arg Ser  
 515 520 525

Ser Ser Met Val Asp Gly Glu Asn Ser Phe His Thr Val Leu Cys Asp  
 530 535 540

Gln Gly Leu Asp Pro Glu Ile Ile Leu Gln Val Phe Lys Gln Leu Phe  
 545 550 555 560

Tyr Met Ile Asn Ala Val Thr Leu Asn Asn Leu Leu Leu Arg Lys Asp  
 565 570 575

Ala Cys Ser Trp Ser Thr Gly Met Gln Leu Arg Tyr Asn Ile Ser Gln  
 580 585 590

Leu Glu Glu Trp Leu Arg Gly Lys Asn Leu His Gln Ser Gly Ala Val  
 595 600 605

Gln Thr Met Glu Pro Leu Ile Gln Ala Ala Gln Leu Leu Gln Leu Lys  
 610 615 620

Lys Lys Thr His Glu Asp Ala Glu Ala Ile Cys Ser Leu Cys Thr Ser  
 625 630 635 640

Leu Ser Thr Gln Gln Ile Val Lys Ile Leu Asn Leu Tyr Thr Pro Leu  
 645 650 655

Asn Glu Phe Glu Glu Arg Val Thr Val Ser Phe Ile Arg Thr Ile Gln  
 660 665 670

Ala Gln Leu Gln Glu Arg Asn Asp Pro Gln Gln Leu Leu Leu Asp Ser  
 675 680 685

Lys His Val Phe Pro Val Leu Phe Pro Tyr Asn Pro Ser Ala Leu Thr  
 690 695 700

Met Asp Ser Ile His Ile Pro Ala Cys Leu Asn Leu Glu Phe Leu Asn  
 705 710 715 720

Glu Val

<210> 123

<211> 549

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
 BAR gene sequence

<220>

<221> CDS

<222> (1)..(549)

<400> 123

agc cca gaa cga cgc ccg gcc gac atc cgc cgt gcc acc gag gcg gac 48  
 Ser Pro Glu Arg Arg Pro Ala Asp Ile Arg Arg Ala Thr Glu Ala Asp  
 1 5 10 15

atg ccg gcg gtc tgc acc atc gtc aac cac tac atc gag aca agc acg 96  
 Met Pro Ala Val Cys Thr Ile Val Asn His Tyr Ile Glu Thr Ser Thr  
 20 25 30

gtc aac ttc cgt acc gag ccg cag gaa ccg cag gag tgg acg gac gac 144  
 Val Asn Phe Arg Thr Glu Pro Gln Glu Pro Gln Glu Trp Thr Asp Asp  
 35 40 45

ctc gtc cgt ctg cgg gag cgc tat ccc tgg ctc gtc gcc gag gtg gac 192  
 Leu Val Arg Leu Arg Glu Arg Tyr Pro Trp Leu Val Ala Glu Val Asp  
 50 55 60

ggc gag gtc gcc ggc atc gcc tac gcg ggc ccc tgg aag gca cgc aac 240  
 Gly Glu Val Ala Gly Ile Ala Tyr Ala Gly Pro Trp Lys Ala Arg Asn  
 65 70 75 80

gcc tac gac tgg acg gcc gag tcg acc gtg tac gtc tcc ccc cgc cac 288  
 Ala Tyr Asp Trp Thr Ala Glu Ser Thr Val Tyr Val Ser Pro Arg His  
 85 90 95

cag cgg acg gga ctg ggc tcc acg ctc tac acc cac ctg ctg aag tcc 336  
 Gln Arg Thr Gly Leu Gly Ser Thr Leu Tyr Thr His Leu Leu Lys Ser  
 100 105 110  
  
 ctg gag gca cag ggc ttc aag agc gtg gtc gct gtc atc ggg ctg ccc 384  
 Leu Glu Ala Gln Gly Phe Lys Ser Val Val Ala Val Ile Gly Leu Pro  
 115 120 125  
  
 aac gac ccg agc gtg cgc atg cac gag gcg ctc gga tat gcc ccc cgc 432  
 Asn Asp Pro Ser Val Arg Met His Glu Ala Leu Gly Tyr Ala Pro Arg  
 130 135 140  
  
 ggc atg ctg cgg gcg gcc ggc ttc aag cac ggg aac tgg cat gac gtg 480  
 Gly Met Leu Arg Ala Ala Gly Phe Lys His Gly Asn Trp His Asp Val  
 145 150 155 160  
  
 ggt ttc tgg cag ctg gac ttc agc ctg ccg gtg ccg ccc cgt ccg gtc 528  
 Gly Phe Trp Gln Leu Asp Phe Ser Leu Pro Val Pro Pro Arg Pro Val  
 165 170 175  
  
 ctg ccc gtc acc gaa atc tga 549  
 Leu Pro Val Thr Glu Ile  
 180

<210> 124

<211> 182

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
BAR gene sequence

<400> 124

Ser Pro Glu Arg Arg Pro Ala Asp Ile Arg Arg Ala Thr Glu Ala Asp  
 1 5 10 15

Met Pro Ala Val Cys Thr Ile Val Asn His Tyr Ile Glu Thr Ser Thr  
 20 25 30

Val Asn Phe Arg Thr Glu Pro Gln Glu Pro Gln Glu Trp Thr Asp Asp  
 35 40 45

Leu Val Arg Leu Arg Glu Arg Tyr Pro Trp Leu Val Ala Glu Val Asp  
 50 55 60

Gly Glu Val Ala Gly Ile Ala Tyr Ala Gly Pro Trp Lys Ala Arg Asn  
 65 70 75 80

Ala Tyr Asp Trp Thr Ala Glu Ser Thr Val Tyr Val Ser Pro Arg His  
 85 90 95

Gln Arg Thr Gly Leu Gly Ser Thr Leu Tyr Thr His Leu Leu Lys Ser  
 100 105 110

Leu Glu Ala Gln Gly Phe Lys Ser Val Val Ala Val Ile Gly Leu Pro  
 115 120 125

Asn Asp Pro Ser Val Arg Met His Glu Ala Leu Gly Tyr Ala Pro Arg  
 130 135 140

Gly Met Leu Arg Ala Ala Gly Phe Lys His Gly Asn Trp His Asp Val  
 145 150 155 160

Gly Phe Trp Gln Leu Asp Phe Ser Leu Pro Val Pro Pro Arg Pro Val  
 165 170 175

Leu Pro Val Thr Glu Ile  
 180

<210> 125

<211> 366

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (1)..(363)

<400> 125

atg gga aaa ggt gtg aaa tcc ccg ggg gag aag tca cgc tat gag acc 48  
 Met Gly Lys Gly Val Lys Ser Pro Gly Glu Lys Ser Arg Tyr Glu Thr  
 1 5 10 15

tca ctg aat ctg acc acc aag cgc ttc ctg gag ctg ctg agc cac tcg 96  
 Ser Leu Asn Leu Thr Thr Lys Arg Phe Leu Glu Leu Leu Ser His Ser  
 20 25 30

gct gac ggt gtc gtc gac ctg aac tgg gct gcc gag gtg ctg aag gtg 144  
 Ala Asp Gly Val Val Asp Leu Asn Trp Ala Ala Glu Val Leu Lys Val  
 35 40 45

cag aag cgg cgc atc tat gac atc acc aac gtc ctt gag ggc atc cag 192  
 Gln Lys Arg Arg Ile Tyr Asp Ile Thr Asn Val Leu Glu Gly Ile Gln  
 50 55 60

ctc att gcc aag aag tcc aag aac cac atc cag tgg ctg ggc agc cac 240  
 Leu Ile Ala Lys Lys Ser Lys Asn His Ile Gln Trp Leu Gly Ser His  
 65 70 75 80

acc aca gtg ggc gtc ggc gga cgg ctt gag ggg ttg acc cag gac ctc 288  
 Thr Thr Val Gly Val Gly Gly Arg Leu Glu Gly Leu Thr Gln Asp Leu  
 85 90 95

cga cag ctg cag gag agc gag cag cag ctg gac cac ctg atg aat atc 336  
 Arg Gln Leu Gln Glu Ser Glu Gln Gln Leu Asp His Leu Met Asn Ile  
                   100                                  105                                  110

tgt act acg cag ctg cgc ctg ctc tcc tga 366  
 Cys Thr Thr Gln Leu Arg Leu Leu Ser  
                   115                                  120

<210> 126

<211> 121

<212> PRT

<213> Homo sapiens

<400> 126

Met Gly Lys Gly Val Lys Ser Pro Gly Glu Lys Ser Arg Tyr Glu Thr  
 1                                  5                                  10                                  15

Ser Leu Asn Leu Thr Thr Lys Arg Phe Leu Glu Leu Leu Ser His Ser  
                   20                                  25                                  30

Ala Asp Gly Val Val Asp Leu Asn Trp Ala Ala Glu Val Leu Lys Val  
                   35                                  40                                  45

Gln Lys Arg Arg Ile Tyr Asp Ile Thr Asn Val Leu Glu Gly Ile Gln  
                   50                                  55                                  60

Leu Ile Ala Lys Lys Ser Lys Asn His Ile Gln Trp Leu Gly Ser His  
 65                                  70                                  75                                  80

Thr Thr Val Gly Val Gly Gly Arg Leu Glu Gly Leu Thr Gln Asp Leu  
                   85                                  90                                  95

Arg Gln Leu Gln Glu Ser Glu Gln Gln Leu Asp His Leu Met Asn Ile  
                   100                                  105                                  110

Cys Thr Thr Gln Leu Arg Leu Leu Ser  
                   115                                  120